

ABSTRACT OF THE DISCLOSURE

This invention relates to methods and systems for in silico or bioinformatic modeling of cellular metabolism. The invention includes methods and systems for modeling cellular metabolism of an organism, comprising constructing a flux balance analysis model, and applying constraints to the flux balance analysis model, the constraints selected from the set consisting of: qualitative kinetic information constraints, qualitative regulatory information constraints, and differential DNA microarray experimental data constraints. In addition, the present invention provides for computational procedures for solving metabolic problems.